

10/777,288

<!--StartFragment--> GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: November 3, 2006, 14:02:40 ; Search time 7317 Seconds
(without alignments)
11247.824 Million cell updates/sec

Title: US-10-777-288A-899
Perfect score: 1287
Sequence: 1 gacatctccgtttccctccc.....aaagttaactgactatatg 1287

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 300 summaries

Database : GenEmbl:*
1: gb_env:*
2: gb_pat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
7: gb_sts:*
8: gb_sy:*
9: gb_un:*
10: gb_vi:*
11: gb_ov:*
12: gb_htg:*
13: gb_in:*
14: gb_om:*
15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	1287	100.0	1287	2	CQ850430	CQ850430 Sequence
2	1287	100.0	1287	5	AK127564	AK127564 Homo sapi
3	1283.8	99.8	1370	5	BC073975	BC073975 Homo sapi
4	1062.2	82.5	1496	5	BC016167	BC016167 Homo sapi
5	1062.2	82.5	1556	5	BC064397	BC064397 Homo sapi
6	943.4	73.3	1246	14	BC109937	BC109937 Bos tauru
7	721.2	56.0	1202	6	BC088194	BC088194 Rattus no
8	588.8	45.7	893	6	BC100355	BC100355 Mus muscu
9	487.8	37.9	179531	14	CR933563	CR933563 Wallaby D
10	474	36.8	546	2	CQ722465	CQ722465 Sequence
11	405.2	31.5	29862	5	AL662798	AL662798 Human DNA
12	405.2	31.5	39659	12	CR847874	CR847874 Homo sapi
13	405.2	31.5	71418	5	AL732442	AL732442 Human DNA
14	405.2	31.5	88815	5	CR759778	CR759778 Human DNA
15	405.2	31.5	104755	5	BX908728	BX908728 Human DNA
16	405.2	31.5	105135	5	CR753328	CR753328 Human DNA
c 17	405.2	31.5	110000	5	BA000025_12	Continuation (13 o
c 18	405.2	31.5	110000	5	BA000041_08	Continuation (9 of
19	405.2	31.5	112118	5	BX119957	BX119957 Human DNA
c 20	405.2	31.5	123554	5	AB023049	AB023049 Homo sapi

21	405.2	31.5	130755	5	AL845353	AL845353 Human DNA
22	405.2	31.5	151228	5	AL662800	AL662800 Human DNA
23	405.2	31.5	310542	12	CR752729	CR752729 Homo sapi
24	405.2	31.5	349980	2	CS039417	CS039417 Sequence
25	396	30.8	404	2	AX070414	AX070414 Sequence
c 26	395.6	30.7	110000	5	AB128049_17	Continuation (18 o
27	395.6	30.7	174766	5	AC148659	AC148659 Macaca mu
28	335	26.0	114375	14	AB113357	AB113357 Sus scrof
29	335	26.0	146382	14	AB113356	AB113356 Sus scrof
30	325.2	25.3	473	2	AX982153	AX982153 Sequence
31	325.2	25.3	473	2	BD117012	BD117012 EST and e
32	325.2	25.3	473	2	AR421459	AR421459 Sequence
c 33	302	23.5	634	7	BV238118	BV238118 S234P6240
34	300.8	23.4	504	6	BC058418	BC058418 Mus muscu
c 35	286.8	22.3	437	2	AX335791	AX335791 Sequence
c 36	286.8	22.3	437	2	AX409947	AX409947 Sequence
c 37	285.6	22.2	153274	12	AY555280	AY555280 Mus muscu
38	282.4	21.9	172747	6	AC112970	AC112970 Mus muscu
c 39	282.4	21.9	188873	6	CR974451	CR974451 Mouse DNA
40	273.8	21.3	300	2	BD219935	BD219935 Human gen
c 41	269.4	20.9	349980	2	AX344571	AX344571 Sequence
c 42	269.4	20.9	349980	2	AX344572	AX344572 Sequence
43	253.2	19.7	297409	12	AC096275	AC096275 Rattus no
c 44	253.2	19.7	349943	6	BX883048	BX883048 Rattus no
c 45	229	17.8	21070	5	AB202095	AB202095 Homo sapi
c 46	229	17.8	21071	5	AB088098	AB088098 Homo sapi
47	189.6	14.7	192	2	AX905901	AX905901 Sequence
48	189.6	14.7	192	2	BD041434	BD041434 Sequence
49	189.6	14.7	192	2	AR741695	AR741695 Sequence
50	175.6	13.6	349980	2	AX344552	AX344552 Sequence

<!--EndFragment-->

<!--StartFragment-->GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: November 3, 2006, 13:59:52 ; Search time 918 Seconds
(without alignments)
9774.819 Million cell updates/sec

Title: US-10-777-288A-899
Perfect score: 1287
Sequence: 1 gacatctccgtttccctccc.....aaagttaaactgactatatg 1287

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 300 summaries

Database : N_Geneseq_8:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1287	100.0	1287	13	ADR07393	Adr07393 Full leng
2	1219.8	94.8	1223	12	ADQ87293	Adq87293 Human tum
3	1219.8	94.8	1223	12	ADQ83838	Adq83838 Human tum
4	1059.6	82.3	1243	8	ABX05085	Abx05085 Human nov
5	443.8	34.5	591	13	ADQ53687	Adq53687 Novel can
6	396	30.8	404	5	AAF65130	Aaf65130 Novel hum
7	392	30.5	400	9	ACH16377	Ach16377 Human adu
c 8	298.8	23.2	2036	4	AAD05547	Aad05547 Human sec
9	296.6	23.0	491	14	ADZ61349	Adz61349 Rat g2936
c 10	286.8	22.3	437	6	ABL67963	Abl67963 Ovary can
c 11	286.8	22.3	437	6	ABN96096	Abn96096 Gene #259
c 12	279.8	21.7	457	10	ABT41359	Abt41359 Toxicity
13	273.8	21.3	300	3	AAA01057	Aaa01057 Human col
14	189.6	14.7	192	3	AAC17689	Aac17689 Human sec
c 15	117	9.1	644	5	AAS34255	Aas34255 Human cDN
c 16	70.4	5.5	3133	10	ADC86738	Adc86738 Human GPC
c 17	69.2	5.4	629	13	ACN54594	Acn54594 Cotton an
c 18	69	5.4	3163	10	ADC87060	Adc87060 Human GPC
19	68.8	5.3	28198	10	ADG37080	Adg37080 Mouse pla
20	68.4	5.3	563	5	AAS34384	Aas34384 Human cDN

c	21	66	5.1	5452	10	ADC86736	Adc86736 Human GPC
c	22	65.2	5.1	12733	6	ABK98631	Abk98631 Vector pE
c	23	65.2	5.1	12733	9	ACD13882	Acd13882 L. lactis
c	24	65.2	5.1	12739	6	ABK98592	Abk98592 Vector pE
c	25	65.2	5.1	12739	9	ACD13843	Acd13843 Plasmid p
c	26	65	5.1	1117	10	ADC86688	Adc86688 Human GPC
c	27	64	5.0	588	13	ACN54596	Acn54596 Cotton an
	28	64	5.0	1064	6	ABT09678	Abt09678 Human PAL
	29	62	4.8	500	12	ADP85918	Adp85918 Synthetic
c	30	60.2	4.7	40772	13	ADW39403	Adw39403 Herpes si
c	31	60	4.7	1000	3	AAA02484	Aaa02484 Human col
	32	58.8	4.6	1337	2	AAZ17263	Aaz17263 Human gen
c	33	58.4	4.5	931	11	ACN87435	Acn87435 Breast ca
	34	58.4	4.5	1065	6	ABT09682	Abt09682 Human PAL
	35	57.4	4.5	600	6	ABQ52497	Abq52497 Oligonucl
c	36	57.4	4.5	600	6	ABQ52496	Abq52496 Oligonucl
c	37	57.4	4.5	1459	3	AAA02528	Aaa02528 Human col
	38	56.4	4.4	406	13	ACN59490	Acn59490 Cotton gy
	39	56.2	4.4	53522	6	AAD30228	Aad30228 Human PKD
	40	56.2	4.4	53522	13	ADU03973	Adu03973 Human pol
	41	56.2	4.4	53522	14	AEB35216	Aeb35216 Human Gef
	42	56.2	4.4	53526	2	AAT94101	Aat94101 Human PKD
	43	56.2	4.4	53577	2	AAT18551	Aat18551 Human pol
	44	56.2	4.4	53577	2	AAT94108	Aat94108 Human PKD
	45	56	4.4	4897	2	AAQ03259	Aaq03259 Pseudorab
c	46	55.2	4.3	1416	8	ABZ20967	Abz20967 Animal te
	47	55	4.3	987	6	ABT09669	Abt09669 Human PAL
c	48	54.6	4.2	795	2	AAV55830	Aav55830 FLGA inse
	49	54	4.2	478	13	ACN51281	Acn51281 Cotton an
c	50	54	4.2	799	2	AAV55831	Aav55831 Nucleotid

<!--EndFragment-->

<!--StartFragment-->GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: November 3, 2006, 14:10:30 ; Search time 6938 Seconds
(without alignments)
10373.044 Million cell updates/sec

Title: US-10-777-288A-899
Perfect score: 1287
Sequence: 1 gacatctccgtttccctccc.....aaagttaaactgactatatg 1287

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 300 summaries

Database : EST:*
1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_htc:*
7: gb_est2:*
8: gb_est7:*
9: gb_est8:*
10: gb_est9:*
11: gb_gss1:*
12: gb_gss2:*
13: gb_gss3:*
14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Match	Query Length	DB ID	Description
c	1	883	68.6	985	4 BX340635	BX340635 BX340635
	2	872.8	67.8	876	14 DQ054028	DQ054028 Homo sapi
	3	854.2	66.4	876	14 DQ054029	DQ054029 Pan trogl
	4	846	65.7	1094	3 BM558827	BM558827 AGENCOURT
	5	796.8	61.9	1060	2 BM551645	BM551645 AGENCOURT
	6	730.4	56.8	915	3 BQ954823	BQ954823 AGENCOURT
	7	724.2	56.3	1097	3 BM926246	BM926246 AGENCOURT
	8	721.8	56.1	869	3 BP165929	BP165929 BP165929
	9	709.8	55.2	1288	6 AK145087	AK145087 Mus muscu
	10	709.4	55.1	1151	6 AK172070	AK172070 Mus muscu
	11	702.4	54.6	2082	6 AK038622	AK038622 Mus muscu
	12	675	52.4	675	9 DR157885	DR157885 HESC2_83
c	13	674.8	52.4	739	3 BM677371	BM677371 UI-E-E01-
	14	656.2	51.0	694	2 BI765223	BI765223 603050308
c	15	649.4	50.5	662	7 BF221823	BF221823 7p37b09.x
	16	628.6	48.8	669	2 BI763966	BI763966 603049847
c	17	626.2	48.7	679	7 BF224092	BF224092 7q83g03.x
	18	625.8	48.6	820	9 DN107093	DN107093 1104510 M
c	19	623.8	48.5	819	9 DN106729	DN106729 1104126 M
	20	610.6	47.4	746	10 DT837916	DT837916 LB00441.C
	21	608.8	47.3	746	9 DN871473	DN871473 nad13f12.

	22	594.4	46.2	742	8	CO889119	CO889119	BovGen_17
c	23	589.8	45.8	612	3	BU679422	BU679422	UI-CF-DU1
	24	587.2	45.6	667	2	BI764214	BI764214	603046086
c	25	578.2	44.9	781	9	CX991484	CX991484	DOG_EST_P
	26	576	44.8	576	5	CK825958	CK825958	ik36f08.x
	27	571	44.4	571	9	DA444680	DA444680	DA444680
	28	570.2	44.3	739	6	AY610091	AY610091	Sus scrof
	29	559.8	43.5	806	8	CX218593	CX218593	MNS33196
c	30	550.4	42.8	595	5	CK825959	CK825959	ik36f08.y
	31	546.2	42.4	892	5	CF617102	CF617102	AGENCOURT
	32	546	42.4	976	3	BU513239	BU513239	AGENCOURT
c	33	544	42.3	544	9	DB313908	DB313908	DB313908
c	34	541.2	42.1	749	4	CB321830	CB321830	UI-CF-EN1
	35	535.4	41.6	595	7	AW967384	AW967384	EST379459
	36	535.4	41.6	668	5	CF358996	CF358996	818572 MA
	37	533	41.4	908	5	CF618737	CF618737	AGENCOURT
	38	530	41.2	720	10	DT719601	DT719601	LB0111.CR
	39	526.8	40.9	644	5	CK956234	CK956234	4096335 B
	40	523.8	40.7	527	3	BQ417335	BQ417335	ik36f08.y
	41	521	40.5	521	3	BM790196	BM790196	K-EST0069
c	42	515.4	40.0	518	1	AI143133	AI143133	qb76d09.x
	43	514.2	40.0	627	2	BI837701	BI837701	603086558
	44	512	39.8	773	8	CX239247	CX239247	NMA07043
	45	511.8	39.8	842	4	CA459080	CA459080	AGENCOURT
	46	510.2	39.6	649	5	CK946125	CK946125	4070565 B
	47	509	39.5	631	8	CO894259	CO894259	BovGen_22
	48	507.6	39.4	514	5	CD674180	CD674180	fs07e12.y
	49	504.6	39.2	860	8	CX200108	CX200108	MNS00694
c	50	502	39.0	510	7	BF590482	BF590482	7h35g05.x

<!--EndFragment-->

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<!--StartFragment-->GenCore version 5.1.9
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OM nucleic - protein search, using frame_plus_n2p model

Run on: November 3, 2006, 14:33:07 ; Search time 46.7 Seconds
(without alignments)
3780.113 Million cell updates/sec

Title: US-10-777-288A-899
Perfect score: 2348
Sequence: 1 gacatctccgtttccctccc.....aaagtttaactgactatatg 1287

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 5179358

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 300 summaries

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10777288/runat_03112006_105409_8336/app_query.fasta_1
-DB=A_Geneseq -QFMT=fastan -SUFFIX=n2p.100aligns.rag -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=300 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=100
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-HOST=abss02p -USER=US10777288_@CGN_1_1_364_@runat_03112006_105409_8336
-NCPU=6 -ICPU=3 -NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A_Geneseq 8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	1728	73.6	315	8	ADR09349	Adr09349 Human pro
2	907	38.6	172	6	ABG99987	Abg99987 Human nov
3	243.5	10.4	238	4	ABB68306	Abb68306 Drosophil
4	240	10.2	598	4	ABG14000	Abg14000 Novel hum
5	240	10.2	598	7	ADF60423	Adf60423 Human con
6	219.5	9.3	1216	8	ADX97588	Adx97588 Pancreati
7	219.5	9.3	1250	6	AAO26231	Aao26231 MDDT rela
8	219.5	9.3	1250	8	ADM87156	Adm87156 Human pro
9	209	8.9	763	2	AAW31852	Aaw31852 Mycobacte
10	207.5	8.8	693	7	ADM05164	Adm05164 Human pro

11	207.5	8.8	693	9	AEC88094	Aec88094 Human cDN
12	204.5	8.7	693	5	ABP69529	Abp69529 Human pol
13	203.5	8.7	1008	4	ABB11527	Abb11527 Human apo
14	200	8.5	406	4	ABG27250	Abg27250 Novel hum
15	199	8.5	446	4	ABB70063	Abb70063 Drosophil
16	199	8.5	1579	8	ADS97981	Ads97981 Protein f
17	199	8.5	2161	7	ADJ69477	Adj69477 Human hea
18	199	8.5	2161	9	ADX98562	Adx98562 Human SH3
19	198.5	8.5	598	6	ABU37030	Abu37030 Protein e
20	198.5	8.5	1013	4	ABG08112	Abg08112 Novel hum
21	198	8.4	572	2	AAW31855	Aaw31855 Mycobacte
22	196.5	8.4	313	8	ABO59570	Abo59570 Human gen
23	193.5	8.2	1315	2	AAW76734	Aaw76734 Human mDi
24	193.5	8.2	1616	8	ADP22958	Adp22958 PRO polyp
25	192	8.2	800	8	ABO58564	Abo58564 Human gen
26	191.5	8.2	1248	2	AAy13464	Aay13464 Human dia
27	191.5	8.2	1567	5	ABB99164	Abb99164 Mouse for
28	191.5	8.2	1567	7	ABW01569	Abw01569 Mouse for
29	191.5	8.2	1682	8	ADR14131	Adr14131 Human NF-
30	191	8.1	451	7	ADE62342	Ade62342 Rat Prote
31	190	8.1	639	8	ADN21309	Adn21309 Bacterial
32	188.5	8.0	681	5	ABB93650	Abb93650 Herbicida
c 33	188.5	8.0	684	4	ABG14126	Abg14126 Novel hum
34	187.5	8.0	1006	8	ADU20559	Adu20559 A. thalia
35	187.5	8.0	1006	8	ADU20561	Adu20561 A. thalia
36	187.5	8.0	1526	6	ABO14750	Abo14750 Novel hum
37	187	8.0	1413	5	AAE21729	Aae21729 Human PKI
38	186	7.9	694	5	ABB92421	Abb92421 Herbicida
39	185.5	7.9	280	7	ABW01568	Abw01568 Mouse for
40	183	7.8	325	4	ABG21919	Abg21919 Novel hum
41	183	7.8	386	9	ADZ47759	Adz47759 Mycobacte
42	183	7.8	2091	3	AAB12000	Aab12000 Rat p3103
43	182.5	7.8	1313	7	ADJ70374	Adj70374 Human hea
44	181	7.7	707	9	ADZ44698	Adz44698 NFk-B pro
45	181	7.7	707	9	AEB31351	Aeb31351 Human PSF
46	180.5	7.7	525	9	AEB31354	Aeb31354 Human SFP
47	180.5	7.7	669	9	AEB31352	Aeb31352 Human PSF
48	180.5	7.7	707	4	AAM39141	Aam39141 Human pol
49	180.5	7.7	707	7	ADE54941	Ade54941 Human Pro
50	180.5	7.7	707	7	ADE54938	Ade54938 Human Pro

<!--EndFragment-->

<!--StartFragment-->

GenCore version 5.1.9
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OM nucleic - protein search, using frame_plus_n2p model

Run on: November 3, 2006, 14:44:57 ; Search time 11.1 Seconds
(without alignments)
3346.783 Million cell updates/sec

Title: US-10-777-288A-899
Perfect score: 2348
Sequence: 1 gacatctccgtttccctccc.....aaagtttaactgactatatg 1287

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 300 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10777288/runat_03112006_105413_8382/app_query.fasta_1
-DB=PIR -QFMT=fastan -SUFFIX=n2p.100aligns.rpr -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=300 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=100
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-HOST=abss02p -USER=US10777288_CGN_1_1_71@runat_03112006_105413_8382 -NCPU=6
-ICPU=3 -NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : PIR_80:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query		DB	ID	Description
	Score	Match Length			
1	203.5	8.7	839	2 T04859	extensin homolog F
2	190.5	8.1	577	2 T09024	proline-rich prote
3	187.5	8.0	1006	2 G86292	hypothetical prote
4	185.5	7.9	1690	2 T31670	DNA-directed RNA p
5	181.5	7.7	530	2 A45690	transactivator EBN
c 6	181.5	7.7	682	2 T28899	hypothetical prote
7	181	7.7	990	2 T14756	hypothetical prote
8	180.5	7.7	707	2 A46302	PTB-associated spl
9	180	7.7	416	2 T34279	hypothetical prote
10	180	7.7	1184	2 G01763	atrophin-1 - human
c 11	179.5	7.6	274	2 T25404	hypothetical prote
12	179	7.6	464	2 S22697	extensin - Volvox
13	178	7.6	376	2 S71558	probable cell wall
14	178	7.6	1184	2 S50832	atrophin-1 - human
c 15	177.5	7.6	375	2 JS0427	S-antigen precurs

16	176.5	7.5	786	2	T01456	extensin homolog F
17	176.5	7.5	1255	2	T31065	diaphanous protein
18	176	7.5	473	2	S50755	hypothetical prote
19	176	7.5	708	2	D96711	hypothetical prote
20	174.5	7.4	1188	2	S49915	extensin-like prot
21	174	7.4	1357	2	T29265	hypothetical prote
c 22	173	7.4	1549	2	I48103	type VII collagen
23	172	7.3	1494	2	T14355	protein-tyrosine-p
24	171.5	7.3	350	2	S22456	hydroxyproline-ric
25	171.5	7.3	1611	2	T38236	hypothetical prote
26	171	7.3	666	2	B70803	hypothetical prote
27	171	7.3	1541	2	T02831	AAA protein L4171.
28	170	7.2	620	2	S06733	hydroxyproline-ric
c 29	170	7.2	1489	2	D70807	hypothetical glyci
30	170	7.2	3020	2	A43932	mucin 2 precursor,
31	169.5	7.2	1520	2	T00273	hypothetical prote
32	169	7.2	439	2	S51939	chitinase (EC 3.2.
33	169	7.2	760	2	F86387	probable Pto kinas
34	169	7.2	907	2	E96636	hypothetical prote
35	168.5	7.2	306	2	T52340	cell wall-plasma m
36	168	7.2	515	2	F70904	hypothetical prote
37	167.5	7.1	548	2	S59133	ETS2 repressor fac
c 38	167.5	7.1	1660	2	A70869	hypothetical glyci
39	167.5	7.1	1859	1	A34092	DNA-directed RNA p
40	167.5	7.1	1862	2	T29959	DNA-directed RNA p
41	167	7.1	449	2	S16748	proline-rich prote
42	167	7.1	915	2	T12526	hypothetical prote
43	167	7.1	5262	2	T03454	ALR protein - huma
c 44	166.5	7.1	346	1	S35500	heterogeneous ribo
c 45	166.5	7.1	584	2	G70804	hypothetical glyci
46	165.5	7.0	839	2	F75518	hypothetical prote
47	165.5	7.0	4957	2	T03455	ALR protein - huma
48	165	7.0	487	2	S42442	nuclear protein EB
49	165	7.0	744	2	E86255	hypothetical prote
50	165	7.0	1201	2	G86441	unknow<!--EndFragment-->

```
<!--StartFragment--> GenCore version 5.1.9
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```

OM nucleic - protein search, using frame_plus_n2p model

Run on: November 3, 2006, 14:34:27 ; Search time 83 Seconds
(without alignments)
4302.994 Million cell updates/sec

Title: US-10-777-288A-899
Perfect score: 2348
Sequence: 1 gacatctccgtttccctccc.....aaagttaactgactatatg 1287

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 5699196

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 300 summaries

Command line parameters:

```
-MODEL=frame+_n2p.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10777288/runat_03112006_105411_8347/app_query.fasta_1
-DB=UniProt -QFMT=fastan -SUFFIX=n2p.100aligns.rup -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=300 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=100
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-HOST=abss02p -USER=US10777288 @CGN_1_1_684 @runat_03112006_105411_8347
-NCPU=6 -ICPU=3 -NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
```

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	1716	73.1	315	1	CF136_HUMAN	Q5sqh8 homo sapien
2	1519	64.7	315	2	Q32KT5_BOVIN	Q32kt5 bos taurus
3	1267	54.0	338	2	Q3UM69_MOUSE	Q3um69 mus musculu
4	1256	53.5	326	2	Q3TA61_MOUSE	Q3ta61 mus musculu
5	880	37.5	172	1	CF136_MACMU	Q5tm64 macaca mula
6	792	33.7	172	1	CF136_RAT	Q6mg12 rattus norv
7	788	33.6	172	2	Q497V8_MOUSE	Q497v8 mus musculu
8	476	20.3	102	2	Q6PDX4_MOUSE	Q6pdx4 mus musculu
9	441	18.8	178	2	Q5PPL5_XENTR	Q5ppl5 xenopus tro
10	285.5	12.2	247	2	Q7PFX4_ANOGA	Q7pfx4 anopheles g
11	243.5	10.4	253	2	Q9W1F2_DROME	Q9w1f2 drosophila
12	239.5	10.2	253	2	Q8SYW2_DROME	Q8syw2 drosophila
13	234.5	10.0	3409	2	Q6SSE6_CHLRE	Q6sse6 chlamydomon
14	225	9.6	3889	2	Q6SSE8_CHLRE	Q6sse8 chlamydomon
15	219.5	9.3	1302	1	RAPH1_HUMAN	Q70e73 homo sapien
16	217.5	9.3	4027	2	Q5I2R0_CHLIN	Q5i2r0 chlamydomon
17	217	9.2	2371	2	Q58NA5_CHLIN	Q58na5 chlamydomon
18	212.5	9.1	2332	2	Q4A2B5_9PHYC	Q4a2b5 emiliania h

19	212	9.0	555	1	GP1_CHLRE	Q9fpq6	chlamydomon
20	210.5	9.0	1332	2	Q59GF6_HUMAN	Q59gf6	homo sapien
21	210.5	9.0	1865	2	Q5VU37_HUMAN	Q5vu37	homo sapien
22	210	8.9	665	2	Q2U6Q3_ASPOR	Q2u6q3	aspergillus
23	209	8.9	763	2	Q9XDH2_MYCTU	Q9xdh2	mycobacteri
24	207.5	8.8	585	2	O41935_MHV68	O41935	murid herpe
25	206.5	8.8	727	2	Q35LL9_9BRAD	Q35ll9	bradyrhizob
26	206.5	8.8	745	2	Q89X06_BRAJA	Q89x06	bradyrhizob
27	206	8.8	516	2	Q4A2Z7_9PHYC	Q4a2z7	emiliana h
28	204.5	8.7	616	2	Q9H6K5_HUMAN	Q9h6k5	homo sapien
29	203.5	8.7	839	2	Q9SN46_ARATH	Q9sn46	arabidopsis
30	201.5	8.6	861	2	Q69JZ8_ORYSA	Q69jz8	oryza sativ
31	199	8.5	420	2	Q9VZC2_DROME	Q9vzc2	drosophila
32	199	8.5	2161	1	SHAN1_HUMAN	Q9y566	homo sapien
33	198.5	8.5	598	2	Q8VKN7_MYCTU	Q8vkn7	mycobacteri
34	198.5	8.5	676	2	Q95JC9_PIG	Q95jc9	sus scrofa
35	197.5	8.4	498	2	Q5KGJ5_CRYNE	Q5kgj5	cryptococcu
36	197	8.4	946	2	Q2R063_ORYSA	Q2r063	oryza sativ
37	197	8.4	2033	2	Q9E938_9ALPH	Q9e938	gallid herp
38	197	8.4	2033	2	Q9E940_9ALPH	Q9e940	gallid herp
39	195	8.3	3204	2	Q6X248_9ALPH	Q6x248	bovine herp
40	193.5	8.2	511	2	Q95JD0_PIG	Q95jd0	sus scrofa
41	193.5	8.2	566	2	Q95JD1_PIG	Q95jd1	sus scrofa
42	193.5	8.2	687	2	Q948Y7_VOLCA	Q948y7	volvox cart
43	193.5	8.2	1272	2	Q6URC4_HUMAN	Q6urc4	homo sapien
44	193.5	8.2	1299	2	Q59FH8_HUMAN	Q59fh8	homo sapien
45	191.5	8.2	410	2	Q7PZX2_ANOGA	Q7pzx2	anopheles g
46	191.5	8.2	1248	1	DIAP1_HUMAN	O60610	homo sapien
47	191.5	8.2	1567	1	FMN2_MOUSE	Q9j104	mus musculu
48	191.5	8.2	1682	2	O15054_HUMAN	O15054	homo sapien
49	191	8.1	309	2	Q8UZB4_9VIRU	Q8uzb4	grapevine f
50	191	8.1	451	2	Q62775_RAT	Q62775	rattus norv

<!--EndFragment-->